From:

Leffers, Gerald

Sent:

Tuesday, January 25, 2005 4:06 PM

To:

STIC-Biotech/ChemLib

Subject:

FW:10/776,213 sequence search

Examiner's mailbox is in 2c70 of Remsen. Thank you. Gerry Leffers

Gerald G. Leffers Tr., PhD Primary Examiner, Art Unit 1636 Remsen Building, Room 02A69 (571) 272-0772

-----Original Message-----

From:

Leffers, Gerald

Sent:

Tuesday, January 25, 2005 4:02 PM

To:

STIC-Biotech/ChemLib

Subject:

09/776,213 sequence search

Please do a search/interference search for SEQ ID NO: 2 of this application (~723 nucleotides). Claims are to sequences comprising as few as 17 consecutive nucleotides of SEQ ID NO: 2. Thank you. Gerry Leffers

Gerald G. Leffers Vr., PhD Primary Examiner, Art Unit 1636 Remsen Building, Room 02A69 (571) 272-0772

JAN 25 ZOOS

STAFF USE ONLY

Searcher: ______Searcher Phone: 2Date Searcher Picked up: _____
Date Completed: ______
Searcher Prep/Rev. Time: ____
Online Time: ____

Type of Search

NA Sequence: #______

AA Sequence : #______

Structure: #______

Bibliographic:______

Litigation:______

Patent Family:______

Other:_____

Vendors and cost where applicable
STN:_____
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QUESTEL/ORBIT:____
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Relfield,G.P. and Oakley,C.
Compositions and methods utilizing the yeast ZE01 promoter
Patent: US 6716601-A 2 06-APR-2004;
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Belfield,G.P. and Oakley,C.
Bendield,G.P. and Oakley,C.
Compositions and methods utilizing the yeast ZEO1 promoter
Patent: US 6716601-A 24 06-APR-2004;
Location/Qualifiers
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   CTCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTTATTCCTATCCCGTTGAAGCAACC
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                                                                                                                                                                               100.0%; Score 723; DB 6; 1 larity 100.0%; Pred. No. 6.1e-207; Conservative 0; Mismatches 0;
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/mol_type="genomic
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Sequence 20
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Belfield,G.P. and Oakley,C.
Compositions and methods utilizing the yeast
Patent: US 6716601-A 20 06-APR-2004;
Location/Qualifiers
                                                                                                                                                                                                                                                                                             Unknown.
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                                                                                                                                                                                                                                                                                  Unclassified
                                                                                                                                          Similarity
                                               ACCATAAAGAGCAAAGCGATACCTACTTGGAAGGAAAAGGAGCACGCTTGTAAGGGGGGAT
             GGGGGCTAAGAAGTCATTCACTTTCTTTTCCCTTCGCGGTCCGGACCCCGGGACCCCTCCT
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                                   ACCATAAAGAGCAAAGCGATACCTACTTGGAAGGAAAAGGAGCACGCTTGTAAGGGGGAT
                                                                                              CTTTCGATTAGCACGCACACACATCACATAGACTGCGTCATAAAAATACACTACGGAAAA
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CTCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTTATTCCTATCCCGTTGAAGCAACC
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/mol_type="genomic
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from patent US 6716601.
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100.0%; Pred. No. 6.3e-207;
tive 0; Mismatches 0;
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Sequence
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Belfield,G.P. and Oakley,C.
Compositions and methods utilizing to Patent: US 6716601-A 30 06-APR-2004;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                Unknown
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                                                                                                Score 720.4; DB 6;
Pred. No. 2.4e-206;
0; Mismatches 1;
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                                                                    2 (bases 1 to 23498)
Barrell,B., Rajandream,M.A. and Walsh,S.V.
Direct Submission
Submitted (10-MAR-1995) Saccharomyces cerevisiae chromosome XIII
sequencing project, Sanger Centre, Hinxton Hall, Hinxton, Cambridge
CB10 1RQ E-mail: barrell@sanger.ac.uk
                                                                                                                                                                                                                                                    SC9920 23498 bp DNA S.ceresvisiae chromosome XIII cosmid 9920. 248639 Z71257 Z18639.1 G1:732924 COX7; cytochrome oxidase; delta element; PETIII; transfer RNA-Ala.
              All CDS over 100 codons have been analysed. CDS that are completely overlapped and those that are overlapped by more than 50% of their length by a larger CDS have been omitted from this
                                           Notes:
All CD
                                                                                                                                                                                                                           Saccharomyces cerevisiae Saccharomyces cerevisiae
                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomyces. 1 (bases 1 to 23498)
Hunt,S. and Bowman,S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATAGGGAGGCGCAGTTTATCGGCGGAGCTCTACTTCTTCCTATTTTGGGTAAGCCCCCTTTC
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                                                                                                                                                                                                                                                                    glutamate
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                                                                                                                                                                                                                                                                       decarboxylase;
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600

617 540 557 480

660 677

720

737

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is given for each CDS.
Cosmid 9920 is overlapped at the start of this sequence by cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and at the end of this sequence Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Product="LAKDOWN"
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/xir
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                                                                                                        complement (4197.
                                                                                                                                                   ALAHLCAI YTE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (3200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Saccharomyces c
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/db_xref="taxon:4932"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complement (<1. .2870)
/note="YM9920.01c, unknown, PS00061 Short-chain alcohol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .23498
                                                                                                                                                                                                                                                                                                                                                     start=1
                                                                                                                                                                                                                                                                                                                                                                       .4196,4434. .4505))
known, len: 55, CAI: 0.13, possible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .4196,4691.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    len: 61,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      partial, len: 956, CAI: 0.14; dehydrogenase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .4780))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAI: 0.17, possible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="GA:/02792"

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complement (4685 . .4690)
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complement (4689 . .4694)
/note="possible donor squence, gtcagt"
5632 . .7389
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complement (10777 . 12021)
FSLITAIVSFIĞINTIPSMKFQIPHSKKQWILFGNLGVSGFIFQLLLTMGIQRERAG
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/codon_start=1
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|db_xref="GI:732928"
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Query Match 99.0
Best Local Similarity 99.0
Matches 721; Conservative
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TTTCGATGAGAGAATTAGCAAGCGGAAAAAAACTATGGCTAGCTGGGAGTTGTTTTCAA
                                                                         TGTTTTCGGCCAGTGGTTGCTGCAGGCTGCGCCGGAGAACATAGTGATAAGGGATGTAAC
                                                                                                                                               ATAGGGAGGCGCAGTTTATCGGCGGAGCTCTACTTCCTACTTTCGGTAAGCCCCTTTC
                                                                                                                                                                                                    GTCTCGATAATAGAATAATAAGCGCATTTTTGCTAGCGCCGCCGCGGCGCCCGTTTCCCCA
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TPIIDDEENSIPLTEFDLSDSK"
Complement (12446. .12754)
/note="ym9920.08c, unknown, len: 103, CAI: 0.07,
questionable orf"
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/product="unknown"
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JANSSEN
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Saccharomyces cerevisiae
Saccharomyces cerevisiae
Eukaryota; Fungi; hacomycotta; Saccharomycottina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Bax-responsive
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TGGGACGTCTTAACTTTATTGCAGAGGACTATCAAATCATACAGATATTGTCAAAAAAA
                                                                                                                                                 GTGATAAGGGATGTAACTTTCGATGAGAGAATTAGCAAGCGGAAAAAAACTATGGCTAGC
                                                                                                                                                                                                                       TTGGGTAAGCCCCTTTCTGTTTTCGGCCAGTGGTTGCTGCAGGCTGCGCCGAGAACATA
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                                                                     TGGGAGTTGTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTC
                                                                                                                              GTGATAAGGGATGTAACTTTCGATGAGAGAATTAGCAAGCGGAAAAAAACTATGGCTAGC
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PHARMACEUTICA N.V. (BE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Saccharomyces cerevisiae"
/mol_type="unassigned DNA"
/db_xref="taxon:4932"
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Pred. No. 6.7e-139;
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  Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 257757)
Gardner, M.J., Hall, N., Fung, E., White, O., Berriman, M., Hyman
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                                                                                  complete sequence.
AE014837 AE014186
AE014837.1 GI:234
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Plasmodium falciparum 3D7 chromosome
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Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
Location/Cualifiers
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                                                                                                                                                                                                                                                   CCCCTTTCTGTTTTC 487
                                                                                                                                                                                                                                                                            GTTTCCCAATAGGGAGGCGCAGTTTATCGGCGGAGCTCTACTTCTTCCTATTTGGGTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                            AAGCAACCGCACTATGACTAAATGGTGCTGGACATCTCCATGGCTGTGACTTGTGTGTAT 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garlton, J.M., Pain, A., Nelson, K.E., Bowman, S., Paulsen, I.T., James, K., Bisen, J.A., Rutherford, K., Salzberg, S.L., Craig, A., Kyes, S., Chan, M.-S., Nene, V., Shallom, S.J., Suh, B., Peterson, J., Angiuoli, S., Pertea, M., Allen, J., Selengut, J., Haft, D., Angiuoli, S., Pertea, M., Allen, J., Selengut, J., Haft, D., Mather, M.W., Vaidya, A.B., Martin, D.M.A., Fairlamb, A.H., Fraunholz, M.J., Roos, D.S., Ralph, S.A., McFadden, G.I., Cummings, L.M., Subramanian, G.M., Mungall, C., Venter, J.C., Carucci, D.J., Hoffman, S.L., Newbold, C., Davis, R.W., Fraser, C.M. and Davis, R.W., Fraser, C.M. and
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4159. 4215
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                                                                                                                                                                                                                                                                                                                                                                                                                               501 TGCAGGCTGCGCCGGAGAACATAGTGATAAGGGATGTAACTTTCGATGAGAGAATTAGCA 560
    complete sequence.
BX663508
BX663508.8 GI:40714027
HTG.
                                                                                             BX663508 170295 bp DNA linear VRT 06-JAN-2004
Zebrafish DNA sequence from clone CH211-144B6 in linkage group 22,
                                                                                                                                                                                                                                                                    AATCATACAGATATTGTCAAAAAAAAAAAAAGACTAATAATAACA 722
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YGIPRMYKMLTSYPTYREELINNEKQKSVDIFYIDMGVVIHHCTHANKEKLPIYDEH
ELFSNILQYLKNLFYLIKPKKLIYIGVDGVSPKAKMQQRKRRFLSIFKINDNDNTSN
ELFSNILQYLKNLFYLIKPKKLIYIGVDGVSPKAKMQQRKRRFLSIFKINDNDNTSN
LFNPRCITTGTDFMYKINLSLAKMFKILKKKKYPEFDVIFSGSDVAAGEGEHKILKYIR
ENCKRDSNFKNYNHCIYGLDADLIMLSILVTHLNNIFILSGSDVAAGEGEHKILKYIR
ENCKRDSNFKNYNHCIYGLDADLIMLSILVTHLNNIFILSKFKISDNIFKEINNELEN
TQNTFNNDEYNSFNEQQNDNINYNEEGENDIIKKKKYPEFDVIFKESLINGINSILNEINNEEIN
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NSIKTOIATYINKLKKEKNIVFSISRVVDDIVFLSFLVGNDFLEHIPNIDINEGSNME
ILNSYIFYIKYSNYITYKDKVHIERLKIILKILSAQEFEYFKKGINENISFTDEQ
KYKKYYYLHKFGLEDPKEIQNIVKKYIEGLFWALHYYHFGCASWWEIPHYHYAPLCSD
LLSFEKSDFFFEKYYKKEKLFMGKFYSAFTHLISVLPQKDKNLLPDAYKNIYVEDBVK
LLSFEKSDFFFEKYYKKKEKLFMGKFYSAFTHLISVLPQKDKNLLPDAYKNIYVEDBVK
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/locus tag="PF11_0074" (complement(join(10677. .10818,10922. .10993,11120. .11199, 11295. .11397,11559. .12736,12847. .13503))
/locus tag="PF1_0074" (codon_start=1_0074"
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10454. .10485
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12185. .12400
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12784. .12816
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10372. .10409
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10060. .10092
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protein_id="AAN35663.1
/db_xref="GI:23496001"
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: FMBL; Swy. SWYSSPROT; Tr., TRENBL; Wp:, WORMPER; Information on the WORMPER database can be found at hitp://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the this is found the longest good quality representation will be
                                                                                                                                                                                                                                                                                                        78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml CH211-144B6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                   Similarity
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/clone="CH211-144B6"
/clone_lib="CHORI-211"
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Pred. No. 0.3;
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Homo sapiens BAC clone RP11-107
AC092573 AC015764
AC092573.2 GI:15668084
HTG.
                                                                                                                    Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Sep 19, 2001 this sequence version replaced gi:14916158.
                                                                                                                                                                                                          5 (bases 1 to 171265) Waterston, R.
                                                                                                                                                                                                                                                                         Direct Submission
Submitted (19-SEP-2001) Genome
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Submitted (19-JUL-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
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3 (bases 1 to 171265)
Waterston, R.H.
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Tomlinson, C., Cotton, M.,
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Mammalia; Eutheria; Primates;
1 (bases 1 to 171265)
Sulston, J.E. and Waterston, R.
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                                                                                                                                                                                                                                                             University School of Medicine,
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Center project name: H_NH0001007
Drafting Center: WIBR
                                                    Contact: sapiens@watson.wustl.edu
                                                                    Web site: http://genome.wustl.edu/gsc
                                                                                      Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                              USA
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Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                             Louis,
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., bhred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E.,

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FEATURES
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The clone sequenced to the left is RP11-291G2, 1984 bp overlap; the clone sequenced to the right is RP11-158L8. Actual start of this clone is at base position 105122 of RP11-291G2; actual end is at base position 171265 of RP11-107.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence of AC015764 has been incorporated into AC092573.

Location/Qualifiers

1. .171265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymorphisms have been identified between AC013461, AC015764 and {\tt AC012052}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Data from AC013461, AC073465, AC011667 and AC012052 was used to finish this clone, AC015764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VECTOR: pBACe3.6
                                                                                                                            5244. .6318
/note="match to EST AL537636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="similar to Homo sapiens EST AL524174" (NID:912787667)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
                                                      'note="match to EST
                                                                                               note="match to EST AW814670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                            note="match to EST AW814670
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te="match to EST AL537636
                                                                                                                                                                                                                                                                                                                                                         e="match to EST BE867724
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                      y="L2"
                                                            BE867724
                                                                                               (NID:g7907664)"
                                                                                                                                    (NID:g12801129)"
                                                                                                                                                                                                                                                                                          (NID:g7907664)"
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                                                      (NID:g10316500) "
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Matches 102;
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Best Local Similarity
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TCTGGACTAGGCCTCTCAAGGCTCTTAGAGACGGAGAGAAACAAAGATGGACAAAGAA 55929
                             GCTATAAAAAGGAGAAATTAATCCACACAATCTCACACATTCTGGGAGGAAAAATAAACT
                                                                                                                                                             TTCGATGAGAGAATTAGCAAGCGGAAAAAAACTATGGCTAGCTGGGAGTTGTTTTCAAT 601
                                                                                                                                                                                              Conservative
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6802. .6873
                                                                                                                                                                                                                                                            11902. .12561
/note="similar to Homo sapiens
(NID:g10153317)"
                                                                                                                                                                                                                                                                                                          11754. .11994
/note="similar to
(NID:g8624596)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="match to EST AW814670
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note="match to EST BF155794 (NID:g11050977)"
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                                                                                                                                                                                              Score 43.6; D
Pred. No. 0.34
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          lar to Bos taurus EST BF653485 (NID:g11918617)"
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                                                                                                                                                                                                                                                                                                                                                             to EST AL577910 (NID:g12941490)"
                                                                                                                                                                                                                                                                                                                                                                                              to EST AI347484
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AUTHORS
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ORGANISM
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AC012052/c
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galgan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Heboczky, J., Lieu, C., Locke, K., Maddonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassillev, H., Vo, A., Wheeler, J., Wu, X., Winner, A., and Zody, M.
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       Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Center code: wish
Center code: wish
Center code: wish
Center project Information
Center project name: Li385
Center clone name: 337 F 19
Center clone name: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-primer-amersham; 3% of reads
Chemistry: Dye-primer-amersham; 3% of reads
Assembly program: Phrap; version 0.960731
Censensus quality: 191830 bases at least Q40
Censensus quality: 191830 bases at least Q40
Censensus quality: 19935 bases at least Q20
Insert size: 206529; sum-of-centigs
Quality coverage: 4.0 in Q20 base; agarose-fp
Quality coverage: 4.1 in Q20 base;
Censists of 23 centigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the centigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens chromosome SEQUENCE, 23 unordered AC012052 GI:8576227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 2, clone RP11-337F19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (19-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 21, 2000 this sequence version replaced gi:7321517. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 208729)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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1080: contig of 1080 bp in length
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WORKING DRAFT
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56551: contig of 10079 bp in length
6651: gap of 100 bp
64815: gap of 100 bp
64815: gap of 100 bp
75459: contig of 10644 bp in length
75559: gap of 100 bp
90744: contig of 1585 bp in length
90844: gap of 100 bp
107238: contig of 15394 bp in length
107238: contig of 1537 bp in length
113875: contig of 21537 bp in length
128875: gap of 100 bp
155222: gap of 100 bp
175409: contig of 25887 bp in length
178509: gap of 100 bp
178699: contig of 25887 bp in length
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/db_xref="taxon:9606"
/chromosome="2"
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/clone_lib="RPCI-11 Human Male BAC"
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       'note="assembly_fragment"
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Muzny, D., Arenson, A.D., Adams, C., Brundage, E., Bunac, C.,

Carvelli, K., Chacko, J., Chen, J., Di, W., Ding, Y., Dugan, S.,

Durbin, J., Forcum, J., Ganesh, R., Garcia, C., Goodman, M.,

Gorrell, J.H., Haywood, M., Hernandez, J., Jackson, L., Jin, S.,

Kampal, R., Karpathy, S., Kovar, C., Leal, B., Li, Y., Lichtarge, O.,

Liu, W., Logan, O., Lu, J., Ly, T., Martinez, C., Oswal, G., Perez, L.,

Rashid, N.D., Rowland, K., Savage, L., Scherer, S.E., Shen, H.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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178510. .208729
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90845. .107238
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32506. .38167
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107339. .128875
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22611. .27371
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                     /rpt_family="MER53"
4687. .4829
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                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="X"
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Simon,M., Stovall,K., Timms,K.M., Todd,J., Vo,Q., Williamson,A., Worley,K.C., Yu,W., Chinault,C., Nelson,D. and Gibbs,R.A.

(11-APR-1998) Molecular and Human Genetics, Baylor f Medicine, One Baylor Plaza, Houston, TX 77030, USA

Center, Department of Medicine, One

Submitted (17-SEP-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Submitted (29-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 80659)

Submitted (25-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Aug 25, 1998 this sequence version replaced gi:3402643.
Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.

The repeat regions shown were identified using RepeatMasker by

Sequence similarities were identified using Powerblast by Jinghui

Exon/Intron boundaries of identified genes were chosen if there were canonical splice junctions that maintained sequence continuity across the splice junctions.

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note="overlaps bases 114570. .116568 of clone AC112492"

repeat_region

repeat_region repeat_region

complement (5319. .5358)
/rpt_family="AT_rich"
complement (5853. .5898)
/rpt_family="AT_rich"

complement (5943. .6244)
/rpt_family="MLT1E" complement (6228. .6290)
/rpt_family="MLT1D"

repeat_region repeat_region

complement (6631..6758)
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complement (7635..7690)

_family="(CA)n"

complement (6354. .6624)
/rpt_family="L1MA2"

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                                                                                                                                                                                                                                                                                                                                                                                                 33266 AACATGCTAAGAGATTAACTTAAGTGTTTAATTTTAAGGGAATAACTTGAGCGTTCTGTGC 33207
                                                                                                                                                                                                                                                                           33146 ATGAAAAAAAAAAAAAA 33129
                                                                                                                                                                                                                                                                                                                                                                                                                                                            33326 GAACATAGTTGTCAAGAGTTCAAACTCCGAGTTCAAAGTTAGCATGTTTTTAGAAAATAA 33267
                                                                                                                                                                                                                                                                                                697 AAAAAAAAAAAAGACTAA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 195932)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome X, clone RP11-12D5
                                                                                                                                              195932 bp DNA linear HTG 04-APR-2000 Homo sapiens chromosome X clone RP11-12D5 map X, WORKING DRAFT SEQUENCE, 9 unordered pieces.
                                                                              AC021710.4 GI:7408016
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                       CAGTTTCTGGGACGTCTTAACTTTTATTGCAGAGGACTATCAAATCATACAGATATTGTC 696
                                                                                                                                                                                                                                                                                                                                                                                                                               GGCTAGCTGGGAGTTGTTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGA 636
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ilarity 51.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (35042...35071)
/rpt_family="AT_rich"
complement (35418...35439)
/rpt_family="AT_rich"
complement (38090...38123)
/rpt_family="AT_rich"
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25357. .26294
/rpt_family="MER11B"
complement(26295. .26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt family="MER11A"
complement(32126. .32237)
/rpt familv="/-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="(GAA)n"
32378. .32676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /standard_name="DXS67"
complement(33176. .33223)
/rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family='33998. .34051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="LIPA4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="(TAA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="AluSg"
27578. .27870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (28196. .28279)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="L1P"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard_name="G19948"
db_xref="dbSTS:32826"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family="AluSx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     family="L1PA8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42.8; DB 9;
Pred. No. 0.52;
0; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .28748)
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repeat_region repeat_region

repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region

repeat_region

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complement(14686. .14806)
/rpt_family="FLAM_C"
16732

complement (13783. .14150) /rpt_family="L1PA8"

family="MIR"

complement(12725. .12846)
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complement(12853. .12932)
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complement (10630 . .10701)
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complement (11161 . .11220)
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complement(9663. .10244

family="L1MC4"
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repeat_region

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21094

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19560. .19858 /rpt family="AluSg" complement(20203. .20229) /rpt family="AT_rich" 20350. .20551

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complement(18177. ...

family="L1MA9"

1, 19850

complement (16745. .17110) /rpt_family="L1M4" 17480. .17941

tamily="L2"

family="MLT1C"

repeat_region repeat_region repeat_region

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complement(24998. .25210)
/rpt_family="L1PA8"
25211. .25359

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REFERENCE
AUTHORS
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                            FEATURES
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source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (19-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 4, 2000 this sequence version replaced gi:6939568.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 189137 bases at least Q40
Consensus quality: 192288 bases at least Q30
Consensus quality: 193686 bases at least Q20
Insert size: 190000; agarose-fp
Insert size: 195132; sum-of-contigs
Quality coverage: 5.0 in Q20 bases; agarose-fp
Quality coverage: 4.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will be preserved.
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                                                                                  104625
104725
142394
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Center clone name: 12_D_5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome
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                            ocation/Qualifiers
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                                                                                                                                                                              73482: gap of
104624: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1279: contig of 1279 bp in length 1379: gap of 100 bp 0400: contig of 9021 bp in length
                                                                                                                                                                                                                                                                              yof 100 bp in length contig of 8994 bp in length s94: gap of 100 bp in length of 13086 bp in 100; contig of 100 bp
                                                                                                               4: gap of 3: contig
                                                                                                                                                                                                                                        gap of contig
                                                                                                                                                                     of 100 bp

g of 13086 bp in length

f 100 bp

g of 16370 bp in length

g of 24132 bp in length

f 100 bp

g of 31142 bp in length
                                                  100 bp
of 37669 bp in length
100 bp
of 53439 bp in length.
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                                                                                                                                     REFERENCE
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LOCUS
                                   COMMENT
                                                                                                                                                                                                                                                                                        DEFINITION
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                                                                                                                                                                                                                                                        ACCESSION
                                                                                 AUTHORS
TITLE
JOURNAL
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                               189152 ATGAAAAAAAAAAAAA 189169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   577 GGCTAGCTGGGAGTTGTTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    517 GAACATAGTGATAAGGGATGTAACTTTCGATGAGAGAATTAGCAAGCGGAAAAAAACTAT 576
Submitted (08-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk clone no Mar 12, 2001 this sequence version replaced gi:13092292. During sequence assembly data is compared from overlapping clonwhere differences are found these are annotated as variations
                                                                                                                                                                                                                                                     complete sequence.
AL359542
                                                                                                                                                                                                                                                                                        Human DNA sequence from clone
                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                        AL359542
                                                                                                       Direct Submission
                                                                                                                       leath, P
                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                        AL359542.13
                                                                                                                                       . (bases 1 to 28858)
                                                                                                                                                                                                                                                                                                                                                                                                                      AAAAAAAAAAAAGACTAA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGTITICCTCATCAACCAAAAGAGATAATAAAAAAAAACATAAATCGCACAATCATTGTG 189151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGTTTCTGGGACGTCTTAACTTTTATTGCAGAGGACTATCAAATCATACAGATATTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_fragment"
142494. .195932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment"
104725. .142393
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vector_side:left"
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e RP6-190D15
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ome Xq25-26.1,
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FEATURES source repeat_region Group. Further III. O. together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at IMPORTANT: This sequence is not the entire insert of clone RP6-190D15 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP4-537K23 is at 28759 in this sequence. The true right end of clone RP4-753P9 is at 100 in this sequence. Location Qualifiers http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X constructed by the Sanger Centre Chromosome X mapping Group. Further information can be found at 5914. .6224 /note="AluYb8 repeat: matches 1. .311 of consensus" 11889. .12080 /note="AluSg repeat: 5597. .8469 3076. .3129 /note="27 copies 2 mer tc 77% conserved" /note="L1MB3 repeat: matches 6035. .6127 of consensus" 10464. .10518 /note="7SK repeat: matches 1. .53 of consensus" 818. .9104 note="AluSg1 repeat: matches 1. 758. .8796 note="L1MB8 repeat: matches 6133. map="q25-26.1" clone="RP6-190D15" /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="X" note="AluSg repeat: matches 253. .294 of note="38 copies 2 mer aa 69% conserved" .0287. .10362 note="LIMB8 repeat: matches 4267. .6133 of consensus" note="AluSq repeat: matches 1. note="AluSx repeat: matches 1. .299 of consensus" note="AluY repeat: matches 1. .300 of consensus" clone_lib="RPCI-6" note="24 copies 2 mer gt 72% conserved" note="L2 repeat: matches 2602. .2728 of note="AluSx repeat: matches 5. .302 of consensus" .28858 e="AluSx repeat: matches 1. . 646 .6596 matches 24. .298 of consensus" .312 of consensus" .289 of consensus" .296 of consensus" .6171 of consensus" in this sequence. consensus" of f

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13957. .14317
/note="L1M4 repeat: matches 4795.
               /note="AluSc repeat: matches 1. .306 of consensus" 27397. .27415
                                                                                                                                                                                                                                                                        /note="AluSx repeat: matches 1. .216 of 23986. .24027
                                                                                                                                                                                                                                                                                                                                                                                     23037. .23338
                                                                     note="MER51B
                                                                                                                                                                                                                 note="L1ME repeat:
                                                                                                                                                                                                                                                                                                                                                              note="AluSx repeat: matches 1. .296 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="AluSg repeat: matches 38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15957. .16210
                                                                                                         'note="AluSx repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="Weakly double-stranded"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="TIGGER2 repeat: matches 1.
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                                                                                                                                           note="49 copies 2
                                                                                                                                                                             note="AluSx repeat: matches 1. .312 of consensus"
                                                                                                                                                                                                                                                                                                                          note="L1M4 repeat: matches 5627. .5818 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                note="MIR repeat: matches 115.
                                                                                                                                                                                                                                                                                                                                                                                                                                    note="U6 repeat: matches 1. .30 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="AluY repeat: matches 1. .301 of consensus" 0391. .20689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="L1P4 repeat: matches 5345. .5653 of consensus" 0040. .20339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="L1PA12 repeat: matches 5937. .6158 of consensus"
.9745. .20039
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7111. .17277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="AluSq repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5250. .15315
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                                                                                                                                                                                                                                      note="Alu repeat:
4570. .24787
                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="L1PA8 repeat:
1430. .21459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="33 copies 2 mer aa 68% conserved"
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                                                                                                                                                                                                                                                                                                             3770. .23985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat: matches 1. .299 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat: matches 1. .291 of consensus"
repeat: matches 525. .543 of consensus"
                                                                   repeat: matches 453. .526 of
                                                                                                                                         mer ag 61% conserved"
                                                                                                                                                                                                                                                     matches 259. .298 of consensus"
                                                                                                                                                                                                                   matches 5500.
                                                                                                         matches 1. .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          matches 5489. .6163 of consensus"
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; TT:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP than the feature table with their source databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (26-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jul 29, 2002 this sequence version replaced gi:21727348.
                                                      constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6.
                                                                                                                                                http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-246F18 is from the RPCI-23 Mouse PAC Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 209764)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site:
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/note="L2 repeat: matches 2535. .2736 of consensus"
28662. .28805
/note="MIR repeat: matches 110. .256 of consensus"
                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.sanger.ac.uk
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54; Conservative
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/clone_lib="RPCI-23"
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ALIGNMENTS

AAD07475 standard; DNA; 723 BP 23-NOV-1999; 17-NOV-2000; 2000WO-SE002277. 31-MAY-2001. WO200138549-A1. Saccharomyces cerevisiae. Yeast; promoter; gene expression; fermentable carbon source; glucose; non-fermentable carbon source; ethanol; yeast cell culture; ds. Yeast promoter YMR251WA. 10-AUG-2001 (first entry) AAD07475; (ASTR) ASTRAZENECA AB. 99SE-00004247.

New promoter sequences from Saccharomyces cerevisiae useful for controlling expression of homologous and heterologous nucleic acid expression in yeast cells.

WPI; 2001-367697/38.

Belfield G,

Oakley

Claim 1; Page 67-68; 191pp; English.

The invention relates to yeast promoters that are used to control the expression of homologous and heterologous nucleic acids encoding proteins and polypeptides in yeast cells. The yeast promoters are induced by a fermentable carbon source such as glucose or a non-fermentable carbon source such as glucose or a non-fermentable carbon source such as ethanol or both. Therefore expression of nucleic acid molecules encoding a polypeptide under the control of the novel yeast promoters are regulated by varying the level of a fermentable carbon source or a non-fermentable carbon source or both. The yeast promoters

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Yeast; promoter; gene expression; fermentable carbon source; glucose; non-fermentable carbon source; ethanol; yeast cell culture; pYMRZ51AP plasmid; ds.
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New promoter sequences from Saccharomyces cerevisiae useful for controlling expression of homologous and heterologous nucleic acexpression in yeast cells.

Belfield G,

Oakley

(ASTR) ASTRAZENECA

Example 4; Page 133-143; 191pp; English

The invention relates to yeast promoters that are used to control the expression of homologous and heterologous nucleic acids encoding proteins and polypeptides in yeast cells. The yeast promoters are induced by a fermentable carbon source such as glucose or a non-fermentable carbon source such as ethanol or both. Therefore expression of nucleic acid molecules encoding a polypeptide under the control of the novel yeast promoters are regulated by varying the level of a fermentable carbon source or a non-fermentable carbon source or a non-fermentable carbon source or both. The yeast promoters are useful for, inter alia, the high level production of proteins or polypeptides in yeast cell culture. The present sequence is pYMR251AP plasmid related to the invention. This plasmid contains pPRB1 and yeast YMR251MA promoter

Sequence 11427 BP; 3131 A; 2589 C; 2527 G; 3180 T; 0 U; 0 Other;

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The invention relates to yeast promoters that are used to control the expression of homologous and heterologous nucleic acids encoding proteins and polypeptides in yeast cells. The yeast promoters are induced by a fermentable carbon source such as glucose or a non-fermentable carbon source such as ethanol or both. Therefore expression of nucleic acid molecules encoding a polypeptide under the control of the novel yeast promoters are regulated by varying the level of a fermentable carbon source or a non-fermentable carbon source or both. The yeast promoters
                                                                                                                                                                                                                                                                                                     New promoter sequences from Saccharomyces cerevisiae useful for controlling expression of homologous and heterologous nucleic acexpression in yeast cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae Unidentified.
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                                                                                                                                                                                                                                                     Example 3; Page 88-99; 191pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-367697/38.
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RESULT 4
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Best Local S
Matches 723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13073 BP; 3584 A; 2949 C; 2934 G;
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CAT 738
                          CAT 723
                                                                 TCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGGGACGTCTTAACTTT
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Yeast YMR251WA promoter region.

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Query Match
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                                                                                                                                                                                                                                                                                   Sequence
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polypeptide"
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Pred. No. 6.2e-21
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ABQ76446 standard; cDNA; 680 ВP

ABQ76446;

21-NOV-2002 (first entry)

S. cerevisiae BAX-associated cDNA fragment SEQ ID 317.

vasotropic; vaccine; gene therapy; proliferative disorder; cancer; apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia; neurodegeneration; cell death; ss. Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide; vasotropic; vaccine; gene therapy; proliferative disorder; cancer;

Saccharomyces cerevisiae

WO200264766-A2

22-AUG-2002.

21-DEC-2001; 2001WO-EP015398.

RESULT 5
ABQ76446
ID 76446
ID 76446
ID 76446
AC ABQ7
XX ABQ7
XX Bax;
KW Bax;
KW Vaso
KW apop
KW apop
XW apop
XW neux
XX
OS Sacc
XX
O 22-DEC-2000; 04-JAN-2001; 09-JAN-2001; 2000EP-00870318. 2001EP-00870002. 2001EP-00870003.

(JANC) JANSSEN PHARM NV

S 밁 Ś 밁 S

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This invention describes a novel nucleic acid representing a synthetic CC Bax gene. The Bax gene of the invention is useful for identifying Bax-CC resistant yeast or fungi, identifying, or obtaining and identifying CC candida spp. sequences that are differentially expressed in a pathway CC eventually leading to programmed cell death or identifying inhibitors or inhibitor sequences of Bax-induced cell death. The products of the CC invention have cytostatic, fungicide; immunosuppressive, virucide and CC vasotropic activity and can be used in vaccines or for gene therapy. The CC isolated nucleic acids, polypeptides, pharmaceutical compositions, CC antisense molecules and antibodies are useful as medicaments or in CC preparing a medicament for treating, preventing and/or alleviating CC diseases associated with yeast or fungi or proliferative disorders, such CC as cancer, or for preventing apoptosis in certain diseases. The compounds CC preparing a medicament for modifying the endogenic flora of humans and CC preparing andicament for modifying the endogenic flora of humans and CC fungal infections. Apoptosis raleted diseases include autoimmune disease, CC ischaemia, diseases related with viral infections or neurodegenerations. This sequence represents a polynucleotide associated with the Bax gene CC described in the disclosure of the invention
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AAAAAGACTAATAATAACA 722
                                                                                                                                                                                                                                                                                                         GTGATAAGGGATGTAACTTTCGATGAGAGAATTAGCAAGCGGAAAAAAACTATGGCTAGC
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Pred. No. 1.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2000 BP; 336 A; 265 C; 284 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
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Katagiri F,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a method (M1) for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27;
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F, Quan S,
WRMWRMTRRRWAKKSSRTSRRKKRKWCMRKRKYKRMRGYSRMRSCKRARWMKRCRSGRA 423
                                                     TGGTGCTGGACATCTCCATGGCTGTGACTTGTGTGTATCTCACAGTGGTAACGGCACCGT 314
                                                                                                                                                      TCTTCCTTTCATATCTTCCTTTATTCCCATCCCGTTGAAGCAACCGCACTATGACTAAA
                                                                                                                GGGWRGATRYWGRGYMSRMAMMYKKMYWYRGYKGMKRGWWAGRMMMRSMCRWSKACYYMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 5263; 899pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cooper B,
S, Tao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA; 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  258;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 8; Length 2000; Pred. No. 0.66; SB; Mismatches 248; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fungal infection; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glazebrook J, Goff SA, Whitham S, Xie Z, Zhu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 T; 0 U; 752 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            on. M1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                363
                                                                                                                                                                                                                                                                                   194
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RESULT 7

ABS51325/c

ID ABS51325/c

ID ABS51325/c

ABS51326/c

ABS5126/c

ABS51326/c

ABS5126/c

ABS5126
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                                                        17-JAN-2001

19-JAN-2001

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19-JAN-2001
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16-JAN-2001;
16-JAN-2001;
17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bursitis; cirrhosis; hepatitis; polycythaemia vera; anaemia; psoriasis; primary thrombocytopenia; cancer; adenocarcinoma; leukaemia; myeloma; sarcoma; immune system disorder; acquired immunodeficiency syndrome; AIDS; allergy; asthma; Crohn's disease; diabetes mellitus; gout; glomerulonephritis; Goodpasture's syndrome; thyroiditis; pancreatitis; plepatitis; multiple sclerosis; osteoporosis; Reiter's syndrome; rheumatoid arthritis; neurological disorder; epilepsy; stroke; dementia; Alzheimer's disease; pick's disease; Huntington's disease; modd; anxiety; Parkinson's disease; central nervous system disorder; mental disorder; schizophrenic disorder; amnesia; Tourette's disorder; transgenic animal;
                                                                                                                                                                                                                                                                                                                        17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secretory polypeptide; SPTM; actinic keratosis; arteriosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA encoding human secretory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABS51325 standard; cDNA; 2311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KYSGRYWTSWYKY 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGAAATTGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTWMYYMSKYTYAKYGSYWRYRYRAWCMYMWRWYYRXRSYMTYMAWYTSSTRMAMTGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YRGKGYYWAGMWMKRYKRMYMYKMMWWYKRKYSKCSWYCKMSYYASCMKSARKAGAKMCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TMGRCRYKKRSGMKRKCRRRRWGRMYRMRWKRYYMSARYTWRYCARKKYSYSAARKARCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WKMGCRGCMTCRMKSYGMMRWKSWKRMASKYKWMSRMYRWRKKKCSRTTMWGKTRGGMMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSKMSAWSKSMRSSRKCRKCASKRSSAKRYAMMGGMTSGSRMSRWKSYTCYWRKWGSMKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGGTTGCTGCAGGCTGCGCCGGAGAACATAGTGATAAGGGATGTAACTTTCGATGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATAATAAGCGCATTTTTGCTAGCGCCGCCGCCGCGCCCCGTTTCCCAATAGGGAGGCGCA-
; 2001US-0262208P.
; 2001US-0262599P.
; 2001US-0262599P.
; 2001US-0262760P.
; 2001US-0263063P.
; 2001US-0263069P.
; 2001US-0263070P.
; 2001US-0263074P.
; 2001US-0263077P.
; 2001US-0263379P.
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2001US-0261979P.
2001US-0261981P.
2001US-0262164P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene;
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The invention describes an isolated polynucleotide a naturally occurring CC polynucleotide sequence at least 90 % identical to it, a polynucleotide CC complementary to it or an RNA equivalent of it. The purified secretory CC polypeptides (SPTM) and polynucleotides are useful in the diagnosis, CC study, prevention or treatment of diseases associated with decreased CC expression of functional SPTM, e.g. actinic keratosis, arteriosclerosis, CC bursitis, cirrhosis, hepatitis, polycythaemia vera, primary CC thrombocytopenia, anaemia, psoriasis, cancers including adenocarcinoma, CC leukaemia, myeloma or sarcoma, immune system disorder such as acquired cimmunodeficiency syndrome (AIDS), allergies, asthma, Crohn's disease, CC diabetes mellitus, plomerulonephritis, Goodpasture's syndrome, gout, CC Hashimoto's thyroiditis, hepatitis, multiple sclerosis, osteoporosis, CC disease, pick's disease, Huntington's disease, dementia, parkinson's CC disease, other developmental disorder of the central nervous system, CC disease, pick's disease, Huntington's disease, dementia, parkinson's CC disease, other developmental disorder of the central nervous system, CC mental disorder including mood, anxiety or schlzophrenic disorder, hybridisation and amplification technologies, e.g. in assessing gene CC expression patterns, to develop a transcript image for a particular cell or tissue, or to create transgenic animals to model human disease. This sequence encodes a human secretory protein isolated in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Panzer SR, L
Dam TC, Liu
Chang SC, Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New purified secretory polypeptides and polynucleotides, useful in the diagnosis, study, prevention or treatment of diseases associated with decreased expression of functional secretory molecules, e.g. AIDS, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 260-261; 340pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INCY-) INCYTE GENOMICS
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Liu TF, Harris
Gerstin EH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Altus CM,
is B, Flores
Peralta CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dufour GE, Hillman V, Daffo A, Mary David MH, Lewis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hillman JL,
A, Marwaha R,
Lewis SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jones
Chen
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δ 밁 Ş 밁 Ś Query Match Best Local S Matches 80 345 **;** 08 Similarity GACTATCAAATCATACAGATATTGTCAAA 699 GGGAGAAATTGTTGCTCACTATGTGACAGTTTTCTGGGACGTCTTAACTTTTATTGCAGAG TAATCATTTCTCATGTTTATATTTTCCAA 197 CAGCTTAGTTTTCTTACTTTTTAAAATAATTTGGGTGATGTTTTAATCTAACTTGGACAT 5.3%; ilarity 53.7%; Conservative 824 A; 325 C; 473 G; **,** Score 38.6; Di Pred. No. 0.94 0; Mismatches .94; DB T; 0 69; 6 Length 2311; Indels Other; 0; Gaps 610 226 670 286 0

Sequence

2311 BP;

689

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RESULT 8
ADT96256/c
ID ADT962
XX ADT962
XX I6-DEC
XX I6-DEC
XX Colon
XX Colon
KW Lomora
KW immuno
XX
            Colon cancer; T cell; tumour protein; C634S; C635S; C637S; C640S; C636S; humoral immune response; cellular immune response; cytostatic; immunostimulant; human; ss.
                                                                                                           16-DEC-2004
                                                                                                                                         ADT96256;
                                                                                                                                                                       ADT96256 standard; cDNA; 544 BP
                                                                             cancer
                                                                             associated human
                                                                                                         (first entry)
                                                                            cDNA sequence #1763.
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The contract of the contract o

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RESULT 9
AAS29224/c
ID AAS29224 standard; DNA; 7736
XX
AC AAS29224;
XX
                                                                                                                                                                                                                                                                                                                                                                 The invention relates to polynucleotide and polypeptide sequences CC associated with cancer, particularly colon cancer. Also disclosed are (i) CC an expression vector comprising the polynucleotide, (ii) a host cell CC transformed or transfected with the expression vector, (iii) an isolated antibody, or its antigen-binding fragment, which specifically binds to CC the polypeptide, (iv) a method of detecting or determining the presence CC of cancer in a patient, (v) a fusion protein comprising at least one of CC the polypeptides (vi) an oligonucleotide that hybridises to the CC polynucleotide sequence under highly stringent conditions, and (vii) a CC method of stimulating and/or expanding T cells specific for a tumour CC of C634S, C637S, C637S, C640S, C636S or one of the potential open reading CC frames (ORFS) of C636S. These polypeptides are encoded by the CC polynucleotide sequences, where both are capable of eliciting a humoral CC analysis, nucleic acid purification, preventing or treating cancer. CC particularly colon cancer. The polynucleotide and polypeptide sequences are also useful in DNA strand invasion, antisense inhibition, mutational CC analysis, nucleic acid purification, isolation of transcriptionally CC active genes, blocking or transcription factor binding, genome cleavage or in situ hybridisation, and as enhancers of transcription or CC biomarkers. This sequence represents a humon colon cancer associated CC cDNA. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at segdata.uspbto.gov
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jiang Y,
Carter D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acids and polypeptides capable of eliciting humoral and/or cellular immune response, useful for diagnosing, preventing or treating cancer, particularly colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-FEB-2001; 2001US-0267400P.
07-FEB-2001; 2001US-0267382P.
11-MAY-2001; 2001US-0290322P.
12-JUL-2001; 2001US-0305265P.
16-AUG-2001; 2001US-0313077P.
                                                                                                                                                                                                                                                                                                                                            Sequence 544 BP; 181 A; 70 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1775; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-2002; 2002US-00066543.
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                                                                                                                                                                    CORIXA CORP.
                                                                                                                                                                                                    TCATTTGAATGTGTGAATTCAATACAGGCTATGTAAAATTTTTTACTAATGTCATTATTTT
                                                                                                                                       TCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTTCTGGGACGTCTTAACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chenault RA, Fanger GR,
                                                                                                                                                                                                                                                                        5.3%;
llarity 57.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xu J, In
Smith CL,
                                                                                                                                                                                                                                                                    Score 38.4; DB Pred. No. 0.55; 0; Mismatches
                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                          73 G; 216 T; 0 U; 4
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L, Durham M,
                                                                                                                                                                                                                                                                                                          DB
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                                                                                                                                                                                                                                                                                                          11;
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Stolk JA;
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                        Length 544;
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14-AUG-2000;
14-AUG-2000;
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21-NOV-2001 (first entry)
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Genomic sequence #67 encoding novel human DNA-binding protein

Human; DNA-binding protein; histone; chromo domain protein; chromatin organisation modifier; Y-box binding protein; DNA organisation; gene transcription; malignant disease; autoimmune disease; rheumatic disease; genetic abnormality; infectious disease; rheumatic disease; neurological anti rheumati plogical disorder; gene therapy; immunomodulatory; anti-HIV; rheumatic; anti microbial; cytostatic; ds.

17-JAN-2001; 2001WO-US001305

18-APR-2000; 19-MAY-2000; 07-JUN-2000;

26-JUL-2000; 2000US-0217496P. 2000US-0218290P. 2000US-0220963P. 2000US-0220964P. 2000US-0205515P.
2000US-0209467P.
2000US-0214886P.
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20-CCT
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# 2000US-0233064P.
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# 2000US-023429P.
# 2000US-0234364P.
# 2000US-023636P.
# 2000US-0246370P.
# 2000US-0246474P.
# 2000US-024652P.
# 2000US-024652P.
# 2000US-024653P.
# 2000US-0249211P.
# 2000US-024921P.
# 2000US-024921P.
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CC The present invention relates to the isolation of novel DNA-binding CC proteins (AAU18154-AAU18281), and CDNA and genomic sequences encoding for CC these proteins. DNA-binding proteins such as histones, chromo (chromatin CC organisation modifier) domain proteins, and y-box binding proteins may CC contribute to diseases resulting from aberrant DNA organisation and/or CC gene transcription. The sequences of the invention are useful in CC screening assays to identify antagonists and/or agonists that may enhance CC in block activities mediated by DNA-binding proteins. Blockers of DNA-CC binding proteins may be useful in treating disorders such as malignant CC diseases (e.g. cancer), autoimmune disorders (e.g. diabetes mellitus), CC rheumatic diseases (e.g. rheumatoid arthritis), genetic abnormalities CC (e.g. cystic fibrosis), infectious diseases (e.g. HIV) and neurological CC disorders (e.g. Alzheimer's disease). The polymuclocide sequences of the CC invention may also be used in gene therapy. AAS29158-AAS29239 represent CC genomic sequences encoding for novel DNA-binding proteins. Note: The Sequence data for this patent did not form part of the printed CC sequence data for this patent did not form part of the printed CC secification, but was obtained in electronic format directly from WIPO CC at fig. vipo.int/pub/published_pct_sequences
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11-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid molecules encoding human secreted chromosomal binding proteins, used in preventing, treating or ameliorating a disorder, Alzheimer's and Parkinson's diseases and cancers.
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; 2000US-0251969P.

; 2000US-0251999P.

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; 2000US-025199P.

; 2000US-0259678P.
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Sequence 7736 BP; 1672 A; 1981 C; 2164 G; 1919 T; 0 U; 0 Other;

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                  TTGAAGCAACCGCACTA
                                       GAAGTACTCCACTCTCCCGAGTCTGCCTTTCCCTCATGGCCTCTGACCTCGCTCCCC
                                                    GGACCCCTCCTCCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTTATTCCTATCCCG
                                                                                GTTCAGGGGATGGATGTAAAGCACACACACAGTTGTTCCCCCCACAGCCGCCCAGATGTG
                                                                                                      GTAAGGGGGATGGGGGCTAAGAAGTCATTCACTTTCTTTTCCCTTCGCGGTCCGGACCCG
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DT 23-JAN-20;
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DNA;

ABA16123;

23-JAN-2002 (first

Human nervous system related polynucleotide SEQ ID NO 8454.

Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;

08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 12-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000;	cardiant; immune disorder; cardiovascular disorder sease; infection; nephrotropic; gene therapy; vacc OUNG-US001334. OUNG-UJ9065P. OUNS-018664P. OUNS-018874P. OUNS-018874P. OUNS-018886P. OUNS-021880P. OUNS-022575P. OUNS-0225	antirheumatic; hepatotropic; cerebroprotective; antiinflammatory antiallergic; antidiabetic; antiulcer; anticonvulsant; antifunga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The mucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and covarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Matches
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                     hyperproliferative disorder; cancer; renal disorder; arrhythmia; acute glomerulonephritis; cardiovascular disorder; respiratory diso Goodpasture's syndrome; neurological disorder; Alzheimer's disease; Parkinson's disease; endocrine disorder; Addison's disease; reproductive system disorder; endometriosis; infectious disease;
                                                                                                                                                     Human; DNA-binding protein; B cell immunodeficiency; autoimmune disorder; severe combined immunodeficiency; rheumatoid arthritis; Crohn's disease; diabetes mellitus; allergy; asthma; inflammatory condition; thrombosis; graft-versus-host disease; blood-related disorder; atherosclerosis;
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11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID
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  infection;
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14-AUG-2000;
14-AUG-2000;
                     Novel DNA-binding protein useful for diagnosis, prognosis, prevention treatment of immune, hyperproliferative, respiratory, cardiovascular, reproductive, endocrine, gastrointestinal and neurological disorders.
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RUBEN S
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gastrointestinal disorder; multiple sclerosis; gene therapy; ds
Ruben SM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a new DNA-binding protein. The invention CC is useful in treating, preventing, diagnosing and/or prognosing CC immunodeficiencies (e.g. B cell immunodeficiencies), severe combined CC immunodeficiencies), autoimmune disorders (theumatoid arthritis, multiple CC sclerosis, diabetes mellitus), allergic reactions and conditions (e.g. CC asthma), inflammatory conditions, graft-versus-host disease, blood-created disorders (thrombosis, atherosclerosis), hyperproliferative CC disorders (e.g. cancer), renal disorders (e.g. acute glomerulonephritis), CC cardiovascular disorders (e.g. arrhythmia), respiratory disorders (c.g. cardiovascular disorders (e.g. arrhythmia), respiratory disorders (c.g. disease), reproductive system disorders (e.g. Alzheimer's CC disease, Parkinson's disease), endocrine disorders (e.g. Alzheimer's CC disease, reproductive system disorders (e.g. endometriosis), infectious CC disease, reproductive system disorders (e.g. endometriosis), infectious CC disease), reproductive system disorders (e.g. endometriosis), infectious CC diseases (e.g. viral, bacterial or fungal infections) and CC gastrointeatinal disorders (e.g. Crohn's disease), reproductive system disorders (e.g. represent, and/or diagnose couseful to stimulate neuronal growth and treat, prevent, and/or diagnose couseful to stimulate neuronal growth and treat, prevent, and/or diagnose couseful to stimulate neuronal growth and treat, prevent, and/or diagnose couseful to stimulate neuronal growth and treat, prevent, and/or diagnose couseful to stimulate neuronal growth and treat, prevent, and/or diagnose couseful to stimulate neuronal growth and treat, prevent, and/or diagnose couseful to stimulate neuronal growth and treat, prevent, and/or diagnose couseful to stimulate neuronal growth and treat, prevent, and/or diagnose couseful to stimulate neuronal growth and treat, prevent, and/or diagnose couseful to stimulate neuronal growth and treat, prevent and the invention. Note:

CC disease (e.g. Crohn's disease), co
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Best Local Sim
Matches 75;
                                                                                                                                                                                                                                                                                                                                Extracellular matrix protein; cytostatic; antibacterial; virucide; neuroprotective; gynaecological; gastrointestinal-Gen; cardiant; cardiovascular-Gen; neptrotropic; antiinflammatory; muscular-Gen; respiratory-Gen; immunosuppressive; cerebroprotective; vasotropic; nootropic; antiallergic; cancer; bacterial infection; viral infection; nootropic; antiallergic; cancer; bacterial infection; viral infection;
                                                                                                                                                                                                                                              neural disorder; immune system disorder; blood disorder; muscular disorder; reproductive disorder; strointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; inflammatory disorder; proliferative disorder; human; gene therapy;
                                            07-MAR-2002; 2002US-00091483.
                                                                                        13-MAR-2003.
                                                                                                                                     US2003049650-A1
                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA from extracellular matrix gene 78 #3.
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Pred. No. 2.9;
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2000US-0235484P.
2000US-0235834P.
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2000US-0228924P.
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2000US-0229503P.
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2000US-0233164P.
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01-NOV-2000

08-NOV-2000

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17-N
New DNA-binding proteins and gene encoding them, useful for diagnosing, treating and/or preventing e.g. neurological, inflammatory, infectious,
                                                            WPI; 2003-605749/57.
P-PSDB; ADC25241.
                                                                                                                                                     HUMAN GENOME
                                                                                                                  Ruben SM,
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RESULT 13
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ID ABV04394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC binds specifically to the protein, diagnosing a pathological condition or Susceptibility to a pathological condition (comprising determining the presence or absence of a mutation in the nucleic acid and diagnosing a CC condition based on the presence or absence of the mutation), diagnosing a CC pathological condition or susceptibility to a pathological condition (comprising determining the presence or amount of expression of the CC protein in a biological sample and diagnosing a condition based on the CC presence or amount of expression of the protein, preventing, treating or CC ameliorating a medical condition by administering the nucleic acid or protein to a mammalian subject, identifying a binding partner to the CC protein to a mammalian subject, identifying a binding partner to the corresponding to the cDNA sequence, and identifying an activity in a biological assay (comprising expressing the nucleic acid in a cell, isolating the supernatant, detecting an activity in a biological assay and identifying the protein in the supernatant having the control of activity). The nucleic acids and proteins display the following activities Cytostatic, antibacterial, Virucide, Neuroprotective,
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Best Local :
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16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                         20-FEB-2001; 2001WO-US005171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                      23-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                               WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human prostate expression marker cDNA 4385.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
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                                                      ; 2000US-0183319P.
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Pred. No. 2.
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(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC

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Best Local Similarity
Matches 56; Conserv
  31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
19-MAY-2000;
19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                   antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiviral; vulnerary; anticonvulsant; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparastic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder neurological disease; infection; human; secreted protein: musculoskeletal system; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cancer has metastatized in a patient; (f) assessing the prostate cancer has metastatized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient in the aggressiveness or indolence of prostate cancer in a patient.
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for detecting presence
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nilarity 64.4%;
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2000US-0217496P.
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2000US-02218290F.
2000US-0224518P.
2000US-0224518P.
2000US-0224519P.
2000US-0225213P.
2000US-0225214P.
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17-NOV-2000;
                                                                 Claim 1;
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ers related to
and also for
                                                                                                                                                                                        HUMAN GENOME
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2000US-0241787P.
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2000US-0241809P.
                                                                 NO 819;
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                                                                                               for
                                                                                     testing and
                                                           781pp + Sequence Listing; English.
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treating, preventing and/ or prognosing musculoskeletal system including musculting and detection e.g. diagnosis. musculoskeletal

The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies he invention relates to (ABB03087-ABB04109) assoc antibodies for

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RESULT 15
ABX58465/c
ID ABX584
XX ABX584
XX ABX584
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31-JAN-2000;
04-FEB-2000;
28-JUN-2000;
07-JUL-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene; 88; musculoskeletal system antigen; cancer; metastasis; re-vascularisation; thrombosis; arteriosclerosis; mineral content; cardiovascular condition, wound; injury; burn; angiogenesis; ulcer; post-operative tissue repair; limb regeneration; neuronal growth; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; AlDS-related complex; chondrocyte growth; bone graft; skin aging; periodontal regeneration; tissue transport; bone graft; skin aging; keratinocyte growth; hair loss; melanocyte growth; cell proliferation; cell growth; organ transplant; cell differentiation; body height; weight; hair colour; eye colour; skin; percentage of adipose tissue; plymentation; cosmetic surgery; metabolism; biorhythm; caricadic rhythm; depression; tendency for violence; pain; reproductive capability; stress; storage capability; fat content; lipid content; protein content;
                                                                                                                                                                                                                                                                                               US2002147140-A1
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                                                                                                                                                                                17-JAN-2001;
                                                                                                                                                                                                                                        10-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                  nutritional component.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 carbohydrate content;
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The invention describes an isolated nucleic acid molecule comprising a sequence encoding musculoskeletal system associated polypeptides useful for detecting disorders, e.g., cancer or cancer metastases, in animals or humans. The nucleic acid: stimulates re-vascularisation of ischaemic tissues associated with conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions; treats wounds due to injuries, burns, post-operative tissue repair, and ulcers; stimulates angiogenesis and limb regenerative tissue repair, and ulcers; stimulates angiogenesis neuronal damage occurring in certain disorders or neurodegenerative conditions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-related complex; stimulates chondrocyte growth, thus they can be used to enhance bone and periodontal regeneration and aid in tissue transports or neurogeneration.
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02-OCT-2000

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                                                                                                                                                                                   Claim
                                                                                                                                                                                                        Isolated nucleic acid molecules encoding musculoskeletal system associated polypeptides, useful for detecting disorders, e.g. cancer.
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P-PSDB; ABU13189.
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CC activate hair-forming cells and promotes melanocyte growth; stimulates
CC growth and differentiation of hematopoietic cells and bone marrow cells
CC when used in combination with other cytokines; maintains organs before
CC transplantation or for supporting cell culture of primary tissues;
CC induces tissue of mesodermal origin to differentiate in early embryos;
CC increases or decreases the differentiation or proliferation of embryonic
CC stem cells, besides, haematopoietic lineage; modulates mammalian
CC characteristics, such as, body height, weight, hair colour, eye colour,
CC skin, percentage of adipose tissue, pigmentation, size, and shape (e.g.,
CC commetic surgery); modulates mammalian metabolism; changes mammal's metal
CC state or physical state by influencing biorhythms, caricadic rhythms,
CC depression, tendency for violence, tolerance for pain, reproductive
CC capabilities, hormonal or endocrine levels, appetite, libido, memory, or
Stress; increases or decreases storage capabilities, fat content, lipid,
CC protein, carbohydrate, vitamins, minerals, cofactors or other nutritional
CC components. This sequence encodes a novel human musculoskeletal system
CC stress; hortonal or between this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
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Matches 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 printed specification, but wifrom the US patent office at
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AACTCTTTCAATAAANACAGTCATTATACCGTTAAAAAAAAATCCAGATTGATA
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Copyright (c) 1993 - 2005 Compugen Ltd.
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SUMMARIES

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ALIGNMENTS

	FEATURES Source	TITLE JOURNAL COMMENT	ORGANISM REFERENCE AUTHORS	RESULT 1 AQ874584/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE
/Organism="Saccharomyces Cerevisiae" /mol_type="genomic DNA" /strain="Y2278 - S288C background, cir(0) rho(0)" /strain="Y2278 - S288C background, cir(0) rho(0)" /db xref="teaxon: 4932" /lab_host="E. coli" /clone lib="mTn-3xHA/lacZ Insertion Library, strain Y2278" /note="Vector: pHSS6-Sal; A yeast genomic DNA library without 2 micron or mitochondrial DNA was prepared in pHSS6-Sal; genomic DNA was size-fractionated (DNA of roughly 2-3 kb in length) prior to cloning. This library was subsequently mutagenized with a mTn-3xHA/lacZ minitransposon containing lacZ, URA3, and tet resistance.	Yale University P.O. Box 208103, New Haven, CT 06520-8103, USA Tel: 203 432 9949 Pax: 203 432 9949 Pax: 203 432 6161 Email: anuj.kumar@yale.edu te of mTn-3xHA/lacZ insertion. Seq primer: GGCCTTCTTTCTTTGAAGTAC Class: transposon-tagged. Location/Qualifiers 1. 434 /organisms="Saccharomyces cerevisiae"	es, S.A., L., Heic, Miller Cale Anal sruption Shed (198	Saccharomyces cerevisiae Eukaryota; Pungi; Ascomycota; Saccharomycetina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces. 1 (bases 1 to 434) Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A.,	AQ874584 434 bp DNA linear GSS 08-NOV-1999 VII1B3 mTn-3xHA/lacZ Insertion Library, strain Y2278 Saccharomyces cerevisiae genomic 5', genomic survey sequence. AQ874584 AQ874584.1 GI:6286828 GSS. Saccharomyces cerevisiae (baker's yeast)

Query Match

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Submitted (07-58P-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
8 seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces thermotolerans, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and varrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
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7EBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                Genomic exploration of the hemiascomycetous yeasts: 5. Saccharomyces bayanus var. uvarum FEBS Lett. 487 (1), 37-41 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bon, E., Neuveglise, C., Aigle, M. and Durrens, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 927)
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T3 end of clone AS0AA007G06 of library AS0AA from strain CLIB 533
of Saccharomyces bayanus, genomic survey sequence.
AL398217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGGGCTAAGAAGTCATTCACTTTCTTTTCCCTTCGCGGTCCGGACCCGGGACCCCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCACTATGA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCATAAAGAGCAAAGCGATACCTACTTGGAAGGAAAAGGAGCACGCTTGTAAGGGGGAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTTCGATTAGCACGCACACACACACATAGACTGCGTCATAAAATACACTACGAAAA
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Pred. No. 6.2e-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Casaregola, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Artiguenave, F.,
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REFERENCE
AUTHORS
TITLE
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VERSION
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CNS0090X/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321;
                                                                                                Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota, Metazoa; Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                    DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19021 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey segmence
                                                   Genoscope.
Direct Submission
                                                                                                                                                                                               GSS.
                                                                                                                                                                                                             AL052985.1
                                                                                                                                                                                                                              fly), genomic survey sequence. AL052985
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                                                                                                                                                                                                                                                                                                                                                                                                                  TAGTGATAAGGGATGTAAC-TTTCGATGAGAGAATTAGCAAGCG 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTIGGGTAAGCCCCTTTCTGTTTTCGGCCAGTGGTTGCTGCAGGCTGCGCCGGAGAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAACAGCAATAGCGACACTGCGGCCCGGAAC--GTTCTCTCTAGATGGTTCTAGAACGCG
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/clone="ASOAA007G06"
/clone_lib="ASOAA"
/note="end : T3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to Saccharomyces cerevisiae ORF YMR251w [strong similarity to YKR076w and YGR154c]"
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/mol type="genomic DNA"
/strain="CLIB 533"
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Pred. No. 6.7e-29;
0; Mismatches 107;
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CC252581/c
                                                                                COMMENT
                                                                                                                                                                                    REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          702 AAAAAAAGACTAATAATAACA 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               441 WTGAAATAAGAGTTTTTATGCTTCTKAAAWGCTGAAATACATWTTCKDWKKGKKGKCSGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   462 ATTTGGGTAAGCCCCTTTCTGTTTTCGGCCAGTGGTTGCTGCAGGCTGCGCCGGAGAACA 521
                                                                                             Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves, Neognathae; Galliformes; Phasianidae; Phasianidae; Gallus.

1 (bases 1 to 1055)

Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R. Gallus gallus BAC End Reads
Unpublished (2003)
              Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                      CC252581 1055 bp DNA CH261-136H21_Sp6.1 CH261 Gallus gallus
                                                                                                                                                                                                                                                                 Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                  genomic survey sequence. CC252581
Insert Length: 182000
                                                                                Contact: Richard K. Wilson
                                                                                                                                                                                                                                                                                                                               CC252581.1 GI:30589331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR19021"
/clone lib="RPCI-98"
/note="end : TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB 9
Pred. No. 0.18,
38; Mismatches
  Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45; DB 9; Length 821;
No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124;
                                                                                                                                                                                                                                                                                                                                                                                      linear (genomic clone
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E CH261-136H21,
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                   /clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
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592 GTTTTTCAATCATATAAAAGGGAGAAATTG
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                                                                                                                                                                             - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Bilaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
Eukaryota; Metazoa; Archropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genome survey sequence SP6 end of BAC BACN37910 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL108171
AL108171.1 GI:5628475
GGS.
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                                                                                                                                                                                                                                                                                                                                                                                                Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI; CH261 Female Chicken library - for library and clone
                   /mol_type="genomic DN
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ordering information: http://www.chori.org/bacpac"
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/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
/clone="CH261-136H21"
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/mol_type="genomic DNA"
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/clone="BACN37F10"
                                                                           /organism="Drosophila melanogaster"
                                                                                                                              Location/Qualifiers
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/clone_lib="CH261"
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                                                                                                                                                                                                                                                                                                                                                                                                     - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster genome survey sequence SP6 end of BACNOSK14 of DrosBAC library from Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoscope.
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Drosophila melanogaster
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AACTATGGDTAAMTTTAWWAATTTTHTAAAGGGAAGAWTTWTTTTTTTTAAGKGGCCTWT
                               AATTGTTGCTCACTATGTGACAGTTTTCTGGGACGTCTTAACTTTTATTGCAGAGGACTAT 676
                                                                    AVYAWRGGGGAATSGMGGAYCKGWAWTTTTYWWAWTWTTTTTTWWTTTKGWAAGMAAMSAA
                                                                                                    AGCAAGCGGAAAAAAACTATGGCTAGCTGGGAGTTGTTTTTCAATCATATAAAAGGGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACAGTTTCTGGGACGTCTTAACTTTTATTGCAGAGGACTATCAAATCATACAGATATTGT 695
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/plasmid="pBeloBAC11"
/note="end : SP6"
                                                                                                                                                                                                                                                                                                 /organism="Drosophila melanogaster"
/mol_type="genomic_DNA"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                        Clone="BACN08K14"
                                                                                                                                         5.8%; Score 41.6; DJ
42.2%; Pred. No. 1.7;
tive 25; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
Library was constructed by R. Haywood. DNA sequencing by:
Washington University Genome Sequencing Center For information
obtaining a clone please contact: L. David Sibley
(sibley@borcim.wustl.edu), Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2001)
Contact: L. David Sibley
WashU Plasmodium EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang, K., Cole, R., Chakrabarti, D., Haywood, R., Clifton, S., Pape, D., Marra, M., Hilier, L., Martin, J., Wylie, T., Dante, M., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Jentes, E., Ronko, I., Tsagareishvili, R., Belaygorod, L., Franklin, C., Carr, L., Grow, A., Maguire, L., Richey, J., Wadkins, J., Kennedy, S., Levinso, D., Waterston, R., Wilson, R. and Sibley, D.

Washu Plasmodium EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 399.
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Possible reversed clone: similarity on wrong strand Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
1 (bases 1 to 436)
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                                                                                                                                                                                      Similarity
                                            TGTTTATTACATATGAAATTTCGATATTATTCCTTTGGAAGGATAATTTTTGTGGGATAAA 196
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TTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGGGACGTC
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                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                            /note="Vector: pBluescript SK plus; Site 1: EcoRI; Site 2: XhoI; The library was constructed by R Haywood. cDNAs were synthesized from ganetocyte poly(A) + RNA by oligo d(T) priming, size-selected and directionally cloned into the EcoRi (5' end) to XhoI (3' end) sites of the Uni-ZAP XR lambda vector (Stratagene). The primary library was mass excised as phagemid using the ExAssist helper phage (Stratagene). Clones were mass excised using the ExAssist helper phage (Stratagene), the phagemids were precitptated with PEG 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH10B cells. Clone Availability: David Sibley, Washington University."
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/lab_host="DH10B (GeneHog, Invitrogen, Inc.)"
/clone_lib="Plasmodium falciparum 3D7 gametocyte cDNA
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/db_xref="taxon:36329"
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57.3%;
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Pred. No. 1.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Phydroidea, Drosophilidae, Drosophila.
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AL098379
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                                                                                                                                                                                                                             GAGAAATTGTTGCTCACTATGTGACAGTTTCTGGGACGTCTTAACTTTTATTGCAGAGGA 672
                                                                                                                                                                                                                                                                                                               WGWGDWRADRTDGARADRAANAKDKDADGKADTDATKTDGWGTTTKADTTDDTDADWWDW 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTDKDTDKTWTDVWADNAGWWTDKDKTKAKKKRTKTDTKKTKTRTGTKKKTDRGMRKTDT
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GKRGDGDRKDKGTGGDGDSKAKGDRAWAWRAKATRAAAAAAATAAKAT
                                                                                                                                                       KDWDWKDADTKAGRKRGWGWKKGGWKKTTKTKKKKKTDKTKTGTDTKWGWKDKWTDKKRD
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
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/plasmid="pBeloBAC11"
/note="end : SP6"
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                                                                                                                                                                                                                                                                                                                                                                        230 TTGAAGCAACCGCAC 244
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Direct Schmission

Submitted (17 NOV-2003) Masahira Hattori, The Institute of Physical Submitted (17 NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9170)

Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC Clones are derived from the mouse BAC library MSMg01 with the mouse with the mouse BAC library MSMg01 with the mouse with the mouse BAC library MSMg01 with the mouse with the with the mouse with the mouse with the mouse with the with 
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BH572702
BH572702.1 GI:17824541
GSS.
                                                                                                                        BOGTD44TF BOGT Brassica oleracea genomic clone BOGTD44, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               library availability, please contact Kuniya Abe Tsukuba Institude, Bio Resource Center, The Institute of Physical and Chemical Research Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                           BH572702
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Mus musculus molossinus DNA,
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Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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: EcoRI
: EcoRI.
Location/Qualifiers
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|mol type="genomic DNA"
|sub_specise="molossinus"
|db_xref="taxon:57486"
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/sex="male"
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wences of Library MSMg01
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                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 791)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101;
                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                 602977180F1 NIH_MGC_12 Homo sapiens
                                                                                                                                                                               Homo sapiens (human)
                                                                                                                                                                                                         BI255759.1 GI:14809497
                                                                                                                                                                                                                             BI255759
                                                                                                                                                                                                                                       mRNA sequence.
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Other GSSs: BOGTD44TR
Contact: Chris Town
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Class: sheared ends.
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DNA is from a doubled haploid provided by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Brassicales; Brassicaceae; Brassica.
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Brassica oleracea
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                                                                                                                                                                                                                                                                                                                                                                                                 ACTAAGTTAGAATTATTTTGCACATATATTAGATATTTTAGTTTTTTGGGTTTTAAATATAA
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 Library Preparation: Life Technologies, Library Arrayed by: Incyte Genomics, Inc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="BOGT"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb
genomic DNA inserted into pHOS1 using BstXI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
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/clone="BOGTD44"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Meopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                         Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of reshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                                                                                                                                                                        Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Welssenbach, J.
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                                                                                                                                                                                                                                                                                           Nat. Genet.
20296633
                                                                                                                                                                                                                                                                                                              Estimate of human gene number provided by using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
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GSS; genome survey sequence.
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Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
plate: LLAM11298 row: o column: 19
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/note="organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."
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/tissue_type="cervical carcinoma
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 3.
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BG628729/c
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Direct Submission

Direct Submission

Submitted (12-APR-2000) Genoscope - Centre National de Sequencage:

BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

- Web: www.genoscope.cns.fr)

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 911
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                                                                                                                                                                                                                                                                                                                                                                 Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 366) van der Hoeven, R.S. and Tanksley, S.D. ESTs from a tomato flower library Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG628729 366 bp mRNA linear EST cC-esfictEt23G13d1 Tomato flower library from a mixture developmental stages Lycopersicon esculentum cDNA clone cC-esfictEt23G13d1, mRNA sequence.
                                                                                                                                                                                                                                            Tel: 607 255 7886
Fax: 607 255 6683
Email: rv19@cornell.edu
                                                                                                                                                                                                                                                                                                        Contact: Rutger S. van der Hoeven
Cornell University
252 Emerson Hall, Ithaca, NY 1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG628729.1 GI:13680202
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                                                                                                                                                                                                                           sequence.
/culTivar="E6203"
/db xref="taxon:4081"
/db xref="taxon:4081"
/clone="cc-esfictEL23G13d1"
/tissue_type="developing flower buds and open flower
/dev stage="48 week old plants"
/lab_hoste-xxock#
/lab_hoste-xxock#
/clone_lib="Tomato flower library from a mixture of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                              organism="Lycopersicon esculentum'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="Genoscope sequence ID : COAG167BB11LP1~end :
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                                                                                                                                           _type="mRNA
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Pred. No. 4.3;
19; Mismatches
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Best Local Similarity
Matches 76; Conserv
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Best Local Similarity
Matches 73; Conserv
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 715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 TGGAAGTTTGATTTGAÄTAATTTTAGTGATÄAAAGGTTTTTTCTTTTTGGGCTAATATGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AU077905 Rice shoot Oryza sativa (japonica clone S5033_8Z, mRNA sequence.
AU077905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rice cDNA from etiolated shoot 
Unpublished (1997)
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Yamamoto, K. and Sasaki, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AU077905.1 GI:5667645
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 81-298-38-7441
                                                                                                                                                                                                                                                                                                                                                                                                                                                           305-8602, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 81-298-38-7468
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 TAATAACA 722
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                                                                                                                                                                                                                                                                                                                                                                                                =' RGP'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pBK_CMV; Site_1: EcoRI; Site_2: XhoI;
Flowers and flower buds were collected from greenhouse
grown plants and used for library construction (CLEL)
                                                                                                                                                                                                                                                                                                             /organism="Oryza sativa
/mol_type="mRNA"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                   /dev_stage="Etiolated shoot (8 days .
/clone_lib="Rice shoot"
/note="Etiolated shoot (8 days old)"
                                                                                                                                                                                                                                                                                 /db_xref="taxon:39947"
/clone="S5033_8Z"
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Pred. No. 4.3;
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Pred. No. 4.1;
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                                                                                                                                                 527 TTÁTGÁÁAÁTÁÁTÁT 542
                                 708 AGACTAATAATAACAT 723
                                                                                                     467 AGTTTCTTAATTTAATAGTATAGAAATATTAATCAATAGATGCTTTTTCTAACAAAAATT 526
                                                                                                                                                                                                           407 AATTAATTAAATAAATATCATTTTGAATAATTTTTTATTGTTAATTGACAGAATCTGAA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0523
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ541311 845 bp DNA linear GSS 14-NOV-2000 ENTDV65TR Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, genomic survey sequence.
AZ541311
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Class: shotgun
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(bases 1 to 845)

Loftus, B., Van Aken, S. and Fraser, C.

Determination of clone end sequences from Entamoeba histolytica

HM1: HMS sheared DNA library
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Entamoeba histolytica
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High quality sequence stop: 612
Location/Qualifiers
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                                                                                                                                                                                                                                               AGTTGTTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGGG 647
                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="Entamoeba histolytica Sheared DNA"
/clone lib="Entamoeba histolytica Sheared DNA"
/notee="Vector: pHOS1, Site_1: BST I; Constructed at The
/notee="Vector: phosphore; DNA was method blamond (clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + imethod used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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/strain="HM1:IMSS"
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Search completed: February 7, 2005, 23:17:23 Job time : 3219 secs

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Title:
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Gapop 10.0 , Gapext 1.0
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Issued_Patents_NA:*

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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*; FIEG. NO. 1.98-229;	ALIGNMENTS T 1 7743-194-2 101601 ERAL INFORMATION: PLICANT: Belfield, Graham PLICANT: Oakley, Caroline FILE OF INVENTION: Compositions and Methods Utilizing of INVENTION: Controlling Nucleic Acid Expression IE REFERENCE: 3526.82543 ERENT APPLICATION NUMBER: US/09/743,194 RRENT FILING DATE: 2001-01-08 MBER OF SEQ ID NOS: 32 FYMARE: Patentin Ver. 2.0 ID NO 2 ENGTH: 723 YPE: DNA RGANISM: Saccharomyces cerevisiae -743-194-2 100.0%; Score 723; DB 4; Lengtry Match 100.0%; Score 723; DB 4; Lengtry Match 100.0%; Score 723; DB 4; Lengtry Match	28 33.8 4.7 4818 3 US-08-817-926-27 29 33.6 4.6 77851 4 US-09-949-016-12508 30 33.6 4.6 77867 4 US-09-949-016-13211 31 33.6 4.6 77867 4 US-09-949-016-13212 32 33.4 4.6 77867 4 US-09-949-016-12509 33 3.4 4.6 312470 4 US-09-949-016-14043 34 33.4 4.6 312470 4 US-09-949-016-14043 35 33.4 4.6 336024 4 US-09-949-016-12373 36 33.2 4.6 828152 4 US-09-949-016-12777 C 38 33 2 4.6 828152 4 US-09-949-016-28524 C 39 33 4.6 601 4 US-09-949-016-28524 C 39 33 4.6 601 4 US-09-949-016-28524 C 40 33 4.6 828152 4 US-09-949-016-17009 41 32.8 4.5 625163 4 US-09-949-016-17576 C 42 32.8 4.5 98567 4 US-09-949-016-17576 43 32.8 4.5 98567 4 US-09-949-016-176934 44 32.8 4.5 30.828 4 US-09-949-016-13939 45 30.8 4.5 30.828 4 US-09-949-016-13939
Indels 0; Gaps 0;	Sequences for n in Yeast	Sequence 27, Appl Sequence 12508, A Sequence 13211, A Sequence 13212, A Sequence 12509, A Sequence 14043, A Sequence 12373, A Sequence 12773, A Sequence 12777, A Sequence 12777, A Sequence 1709, A Sequence 1709, A Sequence 1709, A Sequence 17576, A Sequence 17576, A Sequence 11750, A Sequence 11750, A Sequence 11750, A Sequence 11954, A Sequence 13954, A Sequence 13954, A Sequence 13956, A Sequence 13966, A Sequence 14044, A Sequence 14064, Ap Sequence 14064, Ap

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Sequence 24, Application US/09743194

Patent No. 6716601

GENERAL INFORMATION:

APPLICANT: Belfield, Graham

APPLICANT: Oakley, Carcoline

TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for

TITLE OF INVENTION: Controlling Nucleic Acid Expression in Yeast

FILE REFERENCE: 3526.82543

CURRENT APPLICATION NUMBER: US/09/743,194

CURRENT APPLICATION NUMBER: US/09/743,194

CURRENT FILING DATE: 2001-01-08

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 24

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Best Local Similarity
Matches 723; Conserv
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ORGANISM: Saccharomyces cerevisiae
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APPLICANT: Dakley, Caroline
TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for
TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for
TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for
TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for
TITLE OF INVENTION: ACCHARGE: BASE43
CURRENT APPLICATION NUMBER: US/09/743,194
CURRENT FILING DATE: 2001-01-08
INVENTION OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 13073
TYPE: DAM:
ORGANISM: Saccharomyces cerevisiae
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Patent No. 6716601
GENERAL INFORMATION:
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723; Conserv
CTCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTATTCCTATCCCGTTGAAGCAACC
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                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                   100.0%; Score 723; DB 4;
100.0%; Pred. No. 1.1e-228;
tive 0; Mismatches 0;
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600 554 540 494 480 434 420 374

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300 255 135

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RESULT 4
US-09-743-194-30
; Sequence 30, Application US/09743194
; Patent No. 6716601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Belfield, Graham
APPLICANT: Oakley, Caroline
TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for
TITLE OF INVENTION: Controlling Nucleic Acid Expression in Yeast
FILE REFERENCE: 3526.82543
CURRENT APPLICATION NUMBER: US/09/743,194
CURRENT FILING DATE: 2001-01-08
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 30
LENGTH: 850
TYPE: DNA
CONTROLLED OF TAXABLE PROPERTY OF TAXABLE PATENTING TO TAXABLE PATENTIN
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 721; Conserv
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                    CTCCCCGCACGATTTCTTCCTTTCATATCCTTTTATTCCTATTCCGTTGAAGCAACC
                                                                                                                GGGGGCTAAGAAGTCATTCACTTTTCCTTTTCCCGGGGTCCGGACCCGGGACCCCTCCT
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Pred. No. 1.5e-228;
0; Mismatches 1;
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Patent No. 5670367
GENERAL INFORMATION:
                                                                                                                                                                                                                                                      CITY: Alexandria
STATE: VA
COUNTRY: USA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSES: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
PILING DATE:
ETLING DATE:
APPLICATION NUMBER: EP 91 114 300.6
PILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                               APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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US-08-232-463-14
; ORGANISM: Human US-09-949-016-17445
                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-949-016-17445
                                                                                                                               FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17445, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                              SEQ ID NO 17445
                                                                                               NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                        TYPE: DNA
                                                        LENGTH: 4989
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 CTCACAGTGGTAACGGCACCGTGGCTCGGAAACGGTTCCTTCGTGACAATTCTAGAACAG 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
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US-09-949-016-17442
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US-09-949-016-17442/c
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLING DATE: 2000-10-03
PRIOR APPLING DATE: 60/231,498
PRIOR APPLIATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER: FILING DATE: 2000-09-08
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
                                                                                                                                                                                                           Sequence 16850, Application US/09949016
Patent No. 6812339
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17442
LENGTH: 11440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4464 ĠŤTCAĠĠĠĠĂŤĠĠAŢĠŢAĂĀĠĊĀCĀĊĀĊĀĠŤŤĠŢŤCCCĊĊĊACĀĠĊĊĠĊĊĊĀĠĀĨĠŢĠ
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milarity 54.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37.8; DB Pred. No. 0.36; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62;
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012

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FILE REFERENCE: PZ024P1
CURRENT APPLICATION NUMBER: US/09/369,247
CURRENT FILING DATE: 1999-08-05
EARLIER APPLICATION NUMBER: 60/074,118
EARLIER APPLICATION NUMBER: 60/074,157
EARLIER APPLICATION NUMBER: 60/074,157
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/074,341
EARLIER APPLICATION NUMBER: 60/074,341
EARLIER APPLICATION NUMBER: 60/074,341
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                                                                                                                                                                                                                                                                                                                                                                               EARLIER FILING DATE: 1998-02-09
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 15
LENGTH: 815
                                                                                                                               Query Match
Best Local !
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SEQ ID NO 16850
LENGTH: 16662
TYPE: DNA
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                FEATURE:
NAME/KEY: SITE
LOCATION: (794)
OTHER INFORMATION: n equals a,t,g, or c
-09-369-247-15
                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens FEATURE: RAME/KEY: SITE LOCATION: (406) OTHER INFORMATION: n equ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: 60/074,141
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                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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                                                                      594 TTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGGGACGTCT
similarity 55.1%;
                                      TATCCTGTTATTTAAATGTGAACATTTATTGTACATTCAGTGAGTTATAGTGTTAATAGT
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                                                                                                        Score 35.8; DB Pred. No. 0.34; 0; Mismatches
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Pred. No. 1
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                                                                                                                                          DB 4; Length 815;
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                                                                                                            57; Indels
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US-09-949-016-16144
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US-09-949-016-16144
                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16144
LENGTH: 191433
                                                                                                                                    NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15419
LENGTH: 212449
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Best Local Similarity
Matches 60; Conserv
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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                    NAME/KEY: misc_feature
LOCATION: (1)...(212449)
                                                                      FEATURE:
                                                                                          ORGANISM: Human
                                                                                                                     TYPE: DNA
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o. 6812339
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ilarity 59.4%;
Conservative (
A,T,C
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Pred. No. 12;
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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US-09-949-016-14133/c
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; ORGANISM: Human
US-09-949-016-17592
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                                                  CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                    Sequence 14133, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
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LENGTH: 72992
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Best Local :
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SEQ ID
              NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
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Pred. No. 13;
0; Mismatches
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OF DETECTION
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; NAME/KEY: misc_feature
; LCCATION: (1)...(98962)
; OTHER INFORMATION: n = A,T,C or
US-09-949-016-14133
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; LOCATION: (1)...(102884)
; OTHER INFORMATION: n = A,T,C
US-09-949-016-17100
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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Matches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17100
LENGTH: 102884
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ORGANISM: Human
FEATURE:
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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78405
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                                CATATCTTCCTTT 217
                                                                                                  TCTTTTCCCTTCGCGGTCCGGGACCCGGGACCCCTCCTCCCCGCACGATTTCTTCCTTT
                                                                                                                                                                      TACTTGGAAGGAAAAGGAGCACGCTTGTAAGGGGGGATGGGGGGCTAAGAAGTCATTCACTT
                                                                  TCCCCACCCTTGCCCACACACCCCTGGAACCCCAGCTCTCTAGCAACTATCTCTTTTTTT
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; Pred. No. 13;
0; Mismatches
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US-09-949-016-26160/c

Sequence 26160, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR TILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0

LENGTH: 601

TYPE: DNA

GORANISM: Human

US-09-949-016-26160
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Search completed: February 7, 2005, 23:20:25 Job time : 180 secs
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.

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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length: 2000000000
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US-10-776-213-24

US-10-776-213-30

US-10-776-213-30

US-10-123-155-198

US-10-123-155-198

US-10-146-731-198

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US-10-140-472-198

US-10-141-761-198

US-10-142-885-198
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sequence 168936, Sequence 6815,	4593,	e 2883,	1976,		819,	Sequence 94399, A	25183,	25182,	.,	Sequence 25182, A	Sequence 106895,	10689		1068		4385,	e 333,	333, Ap		Sequence 29921, A	177			Sequence 20, Appl		198,	198,	198,	Sequence 198, App	•	198,

ALIGNMENTS

US-10-776-213-2

밁 Ś 밁 δ 당 S ; TYPE: DNA ; ORGANISM: Saccharomyces cerevisiae US-10-776-213-2 Sequence 2, Application US/10776213

Sequence 2, Application No. US20040142478A1

[GENERAL INFORMATION:

APPLICANT: Astrazeneca AB

TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for Controlling Nucle

TITLE OF INVENTION: Acid Expression

FILE REFERENCE: 3526.82543

CURRENT APPLICATION NUMBER: US/10/776,213

CURRENT PILING DATE: 2004-02-12

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 723

LENGTH: 723 Query Match Best Local Similarity Matches 723; Conserv 121 121 61 723; Conservative 61 ACCATAAAGAGCAAAGCGATACCTACTTGGAAGGAAAAGGAGCACGCTTGTAAGGGGGAT 120 1 CTTTCGATTAGCACGCACACACACATCACATAGACTGCGTCATAAAAATACACTACGGAAAA 60 GGGGGCTAAGAAGTCATTCACTTTCTTTTCCCCTTCGCGGTCCCGGACCCCGGGACCCCTCCT 180 ACCATAAAGAGCAAAGCGATACCTACTTGGAAGGAAAAGGAGCACGCTTGTAAGGGGGAT CTTTCGATTAGCACGCACACACATCACATAGACTGCGTCATAAAAATACACTACGGAAAA 100.0%; Score 723; DB 18; 100.0%; Pred. No. 5.5e-217; tive 0; Mismatches 0; 0; Length 723; Indels 0 Gaps 120 60

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RESULT 2
US-10-776-213-24
; Sequence 24, Application US/10776213
; Publication No. US20040142478A1
; GENERAL INFORMATION:
APPLICANT: AStraZeneca AB
; TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for Controlling 1; TITLE OF INVENTION: Acid Expression
; TITLE OF INVENTION: Acid Expression
; FILE REFERENCE: 3526.82543
; CURRENT APPLICATION NUMBER: US/10/776,213
; CURRENT FILING DATE: 2004-02-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 24
; LENGTH: 11427
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                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
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              ACCATAAAGAGCAAAGCGATACCTACTTGGAAGGAAAAGGAGCACGCTTGTAAGGGGGAT 120
                                                 CTTTCGATTAGCACGCACACACATCACATAGACTGCGTCATAAAATACACTACGGAAAA 60
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                                                                                                       100.0%; Score 723; DB 18; Length 11427; ilarity 100.0%; Pred. No. 2.5e-216; Conservative 0; Mismatches 0; Indels 0;
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RESULT 3
(Sequence 20, Application US/10776213)
(Sequence 20, Application US/10776213)
(Publication No. US20040142478A1)
(GENERAL IMFORMATION:
(GENERAL IMFORMATION: Compositions and Methods Utilizing Sequences for Controlling Nucle TITLE OF INVENTION: Acid Expression
(FILE REFERENCE: 3526.82543)
(CURRENT APPLICATION NUMBER: US/10/776,213)
(CURRENT APPLICATION NUMBER: US/10/776,213)
(CURRENT FILING DATE: 2004-02-12
(NUMBER OF SEQ ID NOS: 32
(SOFTWARE: PatentIn Ver. 2.0)
(SEQ ID NO 20
(LENGTH: 13073)
(TYDE: DNA
(ORGANISM: Saccharomyces cerevisiae)
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                                                                                    Query Match 100.0%; Score 723; DB 18; Best Local Similarity 100.0%; Pred. No. 2.7e-216; Matches 723; Conservative 0; Mismatches 0;
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RESULT 4

US-10-776-213-30

US-10-776-213-30

Sequence 30, Application US/10776213

Publication No. US20040142478A1

GENERAL INFORMATION:
APPLICANT: AstraZeneca AB

TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for Controlling Nucl
TITLE OF INVENTION: Acid Expression
FILE REFERENCE: 3526.82543

CURRENT APPLICATION NUMBER: US/10/776,213

CURRENT FILING DATE: 2004-02-12

NUMBER OF SEQ ID NOS: 32

SOFTWARE: DATE: 2004-02-12

VIMBER OF SEQ ID NOS: 32

SOFTWARE: B50

TYPE: DNA

ORGANISM: Saccharomyces Cerevisiae

US-10-776-213-30
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                                               Similarity 99.1
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                                                            99.6%;
                                               Score 720.4; DB 18;
Pred. No. 4e-216;
0; Mismatches 1;
                                                 Indels
                                                                              Length
                                                                              850;
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RESULT 5
US-10-451-467A-317
; Sequence 317, Application US/10451467A
; Publication No. US20040161840A1
; Publication No. US20040161840A1
; Publication No. US20040161840A1
; GENERAL INFORMATION:
APPLICANT: EBEEHARDT, INES
APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
APPLICANT: REEXWANS, RIEKA JOSEPHINA
TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
TITLE OF INVENTION: YEAST AND FUNGI
FILE REFERENCE: JAB-1667
; CURRENT FILING DATE: 2003-06-19
PRIOR APPLICATION NUMBER: EP 00870318.3
; PRIOR APPLICATION NUMBER: EP 00870318.3
; PRIOR APPLICATION NUMBER: EP 01870002.1
; PRIOR APPLICATION NUMBER: EP 01870003.9
; PRIOR FILING DATE: 2001-01-04
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 732
; SOFTWARE: PatentIn version 3.1
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Sequence 198, Application US/10123155
Publication No. US20030068794A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desoryers, Luc
APPLICANT: Genoyers, Luc
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goodward, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
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        APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330R1C30
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Best Local
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TYPE: DNA
ORGANISM: Saccharomyces cerevisiae
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ENGTH: 680
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                                                                        Watanabe, Colin K
Wood, William
NUMBER: US/10/123,155
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Pred. No. 7.7e-146;
0; Mismatches 1;
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; Sequence 198, Application US/10146731
; Publication No. US20030129692A1
; GENERAL INFORMATION:
; APPLICANT: Baker; Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang

RESULT 7 US-10-146-731-198/c

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; Prior Application remove
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 198
; LENGTH: 1024
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-155-198
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Matches 52
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52; Conserv
DM.S.M.ATMR..
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 198
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CURRENT FILING DATE: 2002-05-15
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ORGANISM: Homo Sapien
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AAGACTAATAATAAC 721
                                 .YBBBCSMAAA.YRA.NG.TWT.RRASK..A.S.DHABWCH...BSA.B.KNS.S.RAT.
                                                                                              GAGTTGTTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGG
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                                                                 Zhang, Zemin
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Gurney, Austin L.
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 198
LENGTH: 1024
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Best Local (
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TYPE: PRT
ORGANISM: Homo
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C168
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CURRENT FILING DATE: 2002-05-06
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GGTAAGCCCCTTTCTGTTTTCGGCCAGTGGTTGCTGCAGGCTGCGCCGGAGAACATAGTG 526
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Gerritsen, Mary E.
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Wood, William
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Desnoyers, Luc
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US-10-141-761-198/c
Sequence 198, Application US/10141761
; Publication No. US20030148432A1
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330R1C198
CURRENT APPLICATION NUMBER: US/10/141,761
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
SEQ ID NO 198
LENGTH: 1024
TYDE: P3024
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                                                                                                                                                                                      CCGGGACCCCTCCTCCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTTATTCCTATC 226
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Godowski, Paul J.
Gurney, Austin L.
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 Query Match
Best Local Similarity
Matches 52; Conserv
                                                                                                                              SEQ ID NO 198
                                                                                                                                        APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C248
CURRENT APPLICATION NUMBER: US/10/142,885
CURRENT FILING DATE: 2002-05-10
Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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Watanabe, Colin K
Wood, William
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Gerritsen, Mary E.
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Filvaroff, Ellen
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DeForge, Laura
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    Conservative
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5.7%; Score 41; DB 16; Length 1024; 7.7%; Pred. No. 0.088; tive 194; Mismatches 429; Indels
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APPLICANT: Beresini, Ma
APPLICANT: DeForge, Lau
APPLICANT: Desnoyers, L
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T: Zhang, Zemin
INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
INVENTION: ACIDS ENCODING THE SAME
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Wood,William
                                                                               Stewart, Timothy A Tumas, Daniel
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Filvaroff, Ellen
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                    AND NUCLEIC
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LENGTH: 1024
TYPE: PRT
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Best Local
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CURRENT APPLICATION NUMBER: US/10/158,790
CURRENT FILING DATE: 2002-05-30
Prior Application removed - See File Wrap
NUMBER OF SEQ ID NOS: 550
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294
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DM.S.M.ATMR...H
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RESULT 12
US-10-137-871-198/c
US-10-137-871-198/c
; Sequence 198, Application US/10137871
; Publication No. US20030207350A1
; GENERAL INFORMATION:
APPLICANT: Barker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura

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TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R(1513
CURRENT APPLICATION NUMBER: US/10/137,871
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 198
LENGTH: 1024
TYPE: PRT
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.YBBBCSMAAA.YRA.NG.TWT.RRASK..A.S.DHABWCH...BSA.B.KNS.S.RAT.
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                                 ATAAGGGATGTAACTTTCGATGAGAGAATTAGCAAGCGGAAAAAAACTATGGCTAGCTGG
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APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICANT: Chang, Zemin
APPLICANT: Chang, Zemin
APPLICANT: Chang, Zemin
TITLE OF INVENTION: SCCRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C188
CURRENT APPLICATION NUMBER: US/10/140,923
CURRENT FILING DATE: 2002-05-07
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 198
LENGTH: 1024
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Best Local :
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APPLICANT: Baker, Kevin P.
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Publication No. US20030207355A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 7.7% 52; Conservative
                                                                       SBDSYNCBB
                                                                                                    GAACAGGGGCTACAGTCTCGATAATAGAATAATAAGCGCATTTTTGCTAGCGCCGCCGCG
                                                                                                                                       BS.B.DNY...H...YWNY.HRNBY.RCA.N.NC..WSCMH.RA.YDD.SMNSBW..T.S
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                                                                                                                                                                                                           RN.KYH..MH..R.TYSTTDW...HM..S.RY.....N...RCTYT.S.THH..CTYNS
                                                                                                                                                                                                                                                CCGTTGAAGCAACCGCACTATGACTAAATGGTGCTGGACATCTCCATGGCTGTGACTTGT 286
                                                                                                                                                                                                                                                                                                                  CCGGGACCCCTCCTCCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTATTCCTATC
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                                 GCGCCCGTTTCCCCAATAGGGAGGCGCAGTTTATCGGCGGAGCTCTACTTCTTCCTATTTG
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Sherwood, Steven
Smith, Victoria
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                                                                     A...W.RSNN..M.TMAMTS.HR..D.
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US-10-141-756-198
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US-10-141-756-198/c
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CURRENT FILING DATE: 2002-05-08
Prior Apploication removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550
SEQ ID NO 198
LENGTH: 1024
TYPE: PRT
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APPLICANT: Berceini, Maure
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Elle:
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Best Local S
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     227
                                     834 ST..DGDMNC.SGT.K.B.YY...D.RST.B.SCN.NNM.WC.M.RAATB.M..R.N..N 775
                                                                                                             894 GA.T....MM.SBTAASD.MKW...WBH.H..SBCAGRB.HYBN...YNYNSS.WHS..A
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                                                                                                                                                   467 GGTAAGCCCCTTTCTGTTTTCGGCCAGTGGTTGCTGCAGGCTGCGCCGGAGAACATAGTG 526
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 CCGTTGAAGCAACCGCACTATGACTAAATGGTGCTGGACATCTCCATGGCTGTGACTTGT 286
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                                                                          CCGGGACCCCTCCTCCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTTATTCCTATC 226
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Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith, Victoria
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                                                        ; ORGANISM: Homo US-10-141-759-198
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US-10-141-759-198/c
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                                                                                          SEQ ID NO 198
LENGTH: 1024
TYPE: PRT
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Query Match
Best Local Similarity
                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/141,759
CURRENT FILING DATE: 2002-05-08
Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baker, Kevin P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCMMRT.WH.BYH.HAT..B..SB.DSST.CH..KB.D.BHA..Y.M.KNWC.R.RH 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTAAGCCCCTTTCTGTTTTCGGCCAGTGGTTGCTGCAGGCTGCGCCCGGAGAACATAGTG 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..AW.HKB...NBRMCNYM.T.S.ANW.HNYTTNCRMD.A.RH..CY.BSDCK.NT.KY 535
                                                                                                                                                                                                                                                                                                Watanabe, Colin K Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gao, Wei-Qiang
Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Desnoyers, Luc
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                       Stewart, Timothy A. Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                   Goddard, Audrey
Godowski, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                              Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                              Sherwood, Steven
                                                                                                                                                                                                                                                                                                                                                                                                               Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beresini, Maureen
5.7%; Score 41; DB 17; 7.7%; Pred. No. 0.088;
                 Length 1024;
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                                                                                                                                        414 ..S.CWN.KTTR.DM.BT.H.M.SR.BM.RH.R...YMA.D.TRHCSCYY.TH.YTR
                                                                                                                                                                                                            474
                                                                                                                                                                                                                                                                         534 ..TTCVMRT.WH.BYH.HAT..B..SB.DSST.CH..KB.D.BHA..Y.M.KNWC.R.RH 475
                                                                                                                                                                                                                                                                                                                                            594 ..AW.HKB...NBRMCNYM.T.S.ANW.HNYTTNCRMD.A.RH..CY..BSDCK.NT.KY 535
                                                                                                                                                                                                                                                                                                                                                                                                           654 SBDSYNCBB.A...W.RSNN..M.TMAMTS.HR..D..A...YN.TAANC..A.B.RCK 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            774 RN.KYH..MH..R.TYSTTDW...HM..S.RY.....N...RCTYT.S.THH..CTYNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              834 ST..DGDMNC.SGT.K.B.YY...D.RST.B.SCN.NNM.WC.M.RAATB.M..R.N..N
                                        707 AAGACTAATAATAAC 721
                                                                       354 YBBBCSMAAA.YRA.NG.TWT.RRASK..A.S.DHABWCH...BSA.B.KNS.S.RAT. 295
                                                                                                       587 GAGTIGTTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGG 646
                                                                                                                                                                                                                                          527 ATAAGGGATGTAACTTTCGATGAGAGAATTAGCAAGCGGAAAAAAACTATGGCTAGCTGG 586
                                                                                                                                                                                                                                                                                                            467 GGTAAGCCCCTTTCTGTTTTCGGCCAGTGGTTGCTGCAGGCTGCGCCCGGAGAACATAGTG 526
                                                                                                                                                                                                                                                                                                                                                                           407 GCGCCCGTTTCCCAATAGGGAGGCGCAGTTTATCGGCGGAGCTCTACTTCTTCCTATTTG 466
                                                                                                                                                                                                                                                                                                                                                                                                                                            347 GAACAGGGGCTACAGTCTCGATAATAGAATAATAAGCGCATTTTTGCTAGCGCCGCCGCG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             714 BS.B.DNY...H...YWNY.HRNBY.RCA.N.NC..WSCMH.RA.YDD.SMNSBW..T.S 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 GTGTATCTCACAGTGGTAACGGCACCGTGGCTCGGAAACGGTTCCTTCGTGACAATTCTA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 CCGTTGAAGCAACCGCACTATGACTAAATGGTGCTGGACATCTCCATGGCTGTGACTTGT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 CCGGGACCCCTCCTCCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTTATTCCTATC 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 894 GA.T...MM.SBTAASD.MKW...WBH.H..SBCAGRB.HYBN...YNYNSS.WHS..A 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 954 T.CRYAN..MWMHY..MWT.HYCD.NYTBD..BH.TH.H.BB.SN.S.N..YN..NYHHS 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52; Conservative 194; Mismatches 429; Indels
DM.S.M.ATMR...H 280
                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               715
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